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RAW SEQUENCE LISTING

DATE: 08/29/2002

PATENT APPLICATION: US/10/088,950A

TIME: 12:34:30

Input Set : A:\P1748R1E.txt

Output Set: N:\CRF3\08292002\J088950A.raw

ENTERED

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3 <110> APPLICANT: De Sauvage, Frederic
4   Grewal, Iqbal
5   Gurney, Austin L.
7 <120> TITLE OF INVENTION: MODULATION OF T CELL DIFFERENTIATION FOR THE TREATMENT
8   OF T HELPER CELL MEDIATED DISEASES
10 <130> FILE REFERENCE: P1748R1E
12 <140> CURRENT APPLICATION NUMBER: US 10/088,950A
13 <141> CURRENT FILING DATE: 2002-03-20
15 <150> PRIOR APPLICATION NUMBER: US 60/160,542
16 <151> PRIOR FILING DATE: 1999-10-20
18 <150> PRIOR APPLICATION NUMBER: PCT/US00/28827
19 <151> PRIOR FILING DATE: 2000-10-18
21 <160> NUMBER OF SEQ ID NOS: 16
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 636
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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32 Lys Leu Ala Leu Leu Pro Leu Leu Trp Val Leu Phe Gln Arg Thr
33           20           25           30
35 Arg Pro Gln Gly Ser Ala Gly Pro Leu Gln Cys Tyr Gly Val Gly
36           35           40           45
38 Pro Leu Gly Asp Leu Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu
39           50           55           60
41 Gly Ala Pro Ser Glu Leu His Leu Gln Ser Gln Lys Tyr Arg Ser
42           65           70           75
44 Asn Lys Thr Gln Thr Val Ala Val Ala Ala Gly Arg Ser Trp Val
45           80           85           90
47 Ala Ile Pro Arg Glu Gln Leu Thr Met Ser Asp Lys Leu Leu Val
48           95          100          105
50 Trp Gly Thr Lys Ala Gly Gln Pro Leu Trp Pro Pro Val Phe Val
51          110          115          120
53 Asn Leu Glu Thr Gln Met Lys Pro Asn Ala Pro Arg Leu Gly Pro
54          125          130          135
56 Asp Val Asp Phe Ser Glu Asp Asp Pro Leu Glu Ala Thr Val His
57          140          145          150
59 Trp Ala Pro Pro Thr Trp Pro Ser His Lys Val Leu Ile Cys Gln
60          155          160          165
62 Phe His Tyr Arg Arg Cys Gln Glu Ala Ala Trp Thr Leu Leu Glu
63          170          175          180
65 Pro Glu Leu Lys Thr Ile Pro Leu Thr Pro Val Glu Ile Gln Asp

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66		185		190		195
68	Leu Glu Leu Ala Thr Gly Tyr Lys Val		Tyr Gly Arg Cys Arg	Met		
69		200		205		210
71	Glu Lys Glu Glu Asp Leu Trp Gly Glu		Trp Ser Pro Ile Leu	Ser		
72		215		220		225
74	Phe Gln Thr Pro Pro Ser Ala Pro Lys		Asp Val Trp Val Ser	Gly		
75		230		235		240
77	Asn Leu Cys Gly Thr Pro Gly Gly Glu		Glu Pro Leu Leu Leu	Trp		
78		245		250		255
80	Lys Ala Pro Gly Pro Cys Val Gln Val		Ser Tyr Lys Val Trp	Phe		
81		260		265		270
83	Trp Val Gly Gly Arg Glu Leu Ser Pro		Glu Gly Ile Thr Cys	Cys		
84		275		280		285
86	Cys Ser Leu Ile Pro Ser Gly Ala Glu		Trp Ala Arg Val Ser	Ala		
87		290		295		300
89	Val Asn Ala Thr Ser Trp Glu Pro Leu		Thr Asn Leu Ser Leu	Val		
90		305		310		315
92	Cys Leu Asp Ser Ala Ser Ala Pro Arg		Ser Val Ala Val Ser	Ser		
93		320		325		330
95	Ile Ala Gly Ser Thr Glu Leu Leu Val		Thr Trp Gln Pro Gly	Pro		
96		335		340		345
98	Gly Glu Pro Leu Glu His Val Val Asp		Trp Ala Arg Asp Gly	Asp		
99		350		355		360
101	Pro Leu Glu Lys Leu Asn Trp Val Arg		Leu Pro Pro Gly Asn	Leu		
102		365		370		375
104	Ser Ala Leu Leu Pro Gly Asn Phe Thr		Val Gly Val Pro Tyr	Arg		
105		380		385		390
107	Ile Thr Val Thr Ala Val Ser Ala Ser		Gly Leu Ala Ser Ala	Ser		
108		395		400		405
110	Ser Val Trp Gly Phe Arg Glu Glu Leu		Ala Pro Leu Val Gly	Pro		
111		410		415		420
113	Thr Leu Trp Arg Leu Gln Asp Ala Pro		Pro Gly Thr Pro Ala	Ile		
114		425		430		435
116	Ala Trp Gly Glu Val Pro Arg His Gln		Leu Arg Gly His Leu	Thr		
117		440		445		450
119	His Tyr Thr Leu Cys Ala Gln Ser Gly		Thr Ser Pro Ser Val	Cys		
120		455		460		465
122	Met Asn Val Ser Gly Asn Thr Gln Ser		Val Thr Leu Pro Asp	Leu		
123		470		475		480
125	Pro Trp Gly Pro Cys Glu Leu Trp Val		Thr Ala Ser Thr Ile	Ala		
126		485		490		495
128	Gly Gln Gly Pro Pro Gly Pro Ile Leu		Arg Leu His Leu Pro	Asp		
129		500		505		510
131	Asn Thr Leu Arg Trp Lys Val Leu Pro		Gly Ile Leu Phe Leu	Trp		
132		515		520		525
134	Gly Leu Phe Leu Leu Gly Cys Gly Leu		Ser Leu Ala Thr Ser	Gly		
135		530		535		540
137	Arg Cys Tyr His Leu Arg His Lys Val		Leu Pro Arg Trp Val	Trp		
138		545		550		555

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140  Glu Lys Val Pro Asp Pro Ala Asn Ser Ser Ser Gly Gln Pro His
141                                560                                565                                570
143  Met Glu Gln Val Pro Glu Ala Gln Pro Leu Gly Asp Leu Pro Ile
144                                575                                580                                585
146  Leu Glu Val Glu Glu Met Glu Pro Pro Pro Val Met Glu Ser Ser
147                                590                                595                                600
149  Gln Pro Ala Gln Ala Thr Ala Pro Leu Asp Ser Gly Tyr Glu Lys
150                                605                                610                                615
152  His Phe Leu Pro Thr Pro Glu Glu Leu Gly Leu Leu Gly Pro Pro
153                                620                                625                                630
155  Arg Pro Gln Val Leu Ala
156                                635
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 623
160 <212> TYPE: PRT
161 <213> ORGANISM: Mus musculus
163 <400> SEQUENCE: 2
164  Met Asn Arg Leu Arg Val Ala Arg Leu Thr Pro Leu Glu Leu Leu
165      1      5      10      15
167  Leu Ser Leu Met Ser Leu Leu Leu Gly Thr Arg Pro His Gly Ser
168      20      25      30
170  Pro Gly Pro Leu Gln Cys Tyr Ser Val Gly Pro Leu Gly Ile Leu
171      35      40      45
173  Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu Glu Thr Pro Pro Val
174      50      55      60
176  Leu Tyr His Gln Ser Gln Lys Tyr His Pro Asn Arg Val Trp Glu
177      65      70      75
179  Val Lys Val Pro Ser Lys Gln Ser Trp Val Thr Ile Pro Arg Glu
180      80      85      90
182  Gln Phe Thr Met Ala Asp Lys Leu Leu Ile Trp Gly Thr Gln Lys
183      95     100     105
185  Gly Arg Pro Leu Trp Ser Ser Val Ser Val Asn Leu Glu Thr Gln
186     110     115     120
188  Met Lys Pro Asp Thr Pro Gln Ile Phe Ser Gln Val Asp Ile Ser
189     125     130     135
191  Glu Glu Ala Thr Leu Glu Ala Thr Val Gln Trp Ala Pro Pro Val
192     140     145     150
194  Trp Pro Pro Gln Lys Ala Leu Thr Cys Gln Phe Arg Tyr Lys Glu
195     155     160     165
197  Cys Gln Ala Glu Ala Trp Thr Arg Leu Glu Pro Gln Leu Lys Thr
198     170     175     180
200  Asp Gly Leu Thr Pro Val Glu Met Gln Asn Leu Glu Pro Gly Thr
201     185     190     195
203  Cys Tyr Gln Val Ser Gly Arg Cys Gln Val Glu Asn Gly Tyr Pro
204     200     205     210
206  Trp Gly Glu Trp Ser Ser Pro Leu Ser Phe Gln Thr Pro Phe Leu
207     215     220     225
209  Asp Pro Glu Asp Val Trp Val Ser Gly Thr Val Cys Glu Thr Ser
210     230     235     240

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212	Gly	Lys	Arg	Ala	Ala	Leu	Leu	Val	Trp	Lys	Asp	Pro	Arg	Pro	Cys
213					245					250					255
215	Val	Gln	Val	Thr	Tyr	Thr	Val	Trp	Phe	Gly	Ala	Gly	Asp	Ile	Thr
216					260					265					270
218	Thr	Thr	Gln	Glu	Glu	Val	Pro	Cys	Cys	Lys	Ser	Pro	Val	Pro	Ala
219					275					280					285
221	Trp	Met	Glu	Trp	Ala	Val	Val	Ser	Pro	Gly	Asn	Ser	Thr	Ser	Trp
222					290					295					300
224	Val	Pro	Pro	Thr	Asn	Leu	Ser	Leu	Val	Cys	Leu	Ala	Pro	Glu	Ser
225					305					310					315
227	Ala	Pro	Cys	Asp	Val	Gly	Val	Ser	Ser	Ala	Asp	Gly	Ser	Pro	Gly
228					320					325					330
230	Ile	Lys	Val	Thr	Trp	Lys	Gln	Gly	Thr	Arg	Lys	Pro	Leu	Glu	Tyr
231					335					340					345
233	Val	Val	Asp	Trp	Ala	Gln	Asp	Gly	Asp	Ser	Leu	Asp	Lys	Leu	Asn
234					350					355					360
236	Trp	Thr	Arg	Leu	Pro	Pro	Gly	Asn	Leu	Ser	Thr	Leu	Leu	Pro	Gly
237					365					370					375
239	Glu	Phe	Lys	Gly	Gly	Val	Pro	Tyr	Arg	Ile	Thr	Val	Thr	Ala	Val
240					380					385					390
242	Tyr	Ser	Gly	Gly	Leu	Ala	Ala	Ala	Pro	Ser	Val	Trp	Gly	Phe	Arg
243					395					400					405
245	Glu	Glu	Leu	Val	Pro	Leu	Ala	Gly	Pro	Ala	Val	Trp	Arg	Leu	Pro
246					410					415					420
248	Asp	Asp	Pro	Pro	Gly	Thr	Pro	Val	Val	Ala	Trp	Gly	Glu	Val	Pro
249					425					430					435
251	Arg	His	Gln	Leu	Arg	Gly	Gln	Ala	Thr	His	Tyr	Thr	Phe	Cys	Ile
252					440					445					450
254	Gln	Ser	Arg	Gly	Leu	Ser	Thr	Val	Cys	Arg	Asn	Val	Ser	Ser	Gln
255					455					460					465
257	Thr	Gln	Thr	Ala	Thr	Leu	Pro	Asn	Leu	His	Ser	Gly	Ser	Phe	Lys
258					470					475					480
260	Leu	Trp	Val	Thr	Val	Ser	Thr	Val	Ala	Gly	Gln	Gly	Pro	Pro	Gly
261					485					490					495
263	Pro	Asp	Leu	Ser	Leu	His	Leu	Pro	Asp	Asn	Arg	Ile	Arg	Trp	Lys
264					500					505					510
266	Ala	Leu	Pro	Trp	Phe	Leu	Ser	Leu	Trp	Gly	Leu	Leu	Leu	Met	Gly
267					515					520					525
269	Cys	Gly	Leu	Ser	Leu	Ala	Ser	Thr	Arg	Cys	Leu	Gln	Ala	Arg	Cys
270					530					535					540
272	Leu	His	Trp	Arg	His	Lys	Leu	Leu	Pro	Gln	Trp	Ile	Trp	Glu	Arg
273					545					550					555
275	Val	Pro	Asp	Pro	Ala	Asn	Ser	Asn	Ser	Gly	Gln	Pro	Tyr	Ile	Lys
276					560					565					570
278	Glu	Val	Ser	Leu	Pro	Gln	Pro	Pro	Lys	Asp	Gly	Pro	Ile	Leu	Glu
279					575					580					585
281	Val	Glu	Glu	Val	Glu	Leu	Gln	Pro	Val	Val	Glu	Ser	Pro	Lys	Ala
282					590					595					600
284	Ser	Ala	Pro	Ile	Tyr	Ser	Gly	Tyr	Glu	Lys	His	Phe	Leu	Pro	Thr

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Output Set: N:\CRF3\08292002\J088950A.raw

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285          605          610          615
287 Pro Glu Glu Leu Gly Leu Leu Val
288          620
290 <210> SEQ ID NO: 3
291 <211> LENGTH: 2646
292 <212> TYPE: DNA
293 <213> ORGANISM: Homo sapiens
295 <220> FEATURE:
296 <221> NAME/KEY: unsure
297 <222> LOCATION: 2433
298 <223> OTHER INFORMATION: unknown base
300 <400> SEQUENCE: 3
301 gtgggttcgg ctccccgttg cgcctcgggg gctgtaccca gagctcgaag 50
303 aggagcagcg cggcccgac ccggcaaggc tgggccggac tcggggctcc 100
305 cgagggacgc catgcgggga ggcaggggcg cccctttctg gctgtggccg 150
307 ctgcccagc tggcgtgct gcctctgttg tgggtgcttt tccagcggac 200
309 gcgtccccag ggcagcgcg gccactgca gtgctacgga gttggaccct 250
311 tgggcgactt gaactgctcg tgggagcctc ttggggacct gggagccccc 300
313 tccgagttac acctccagag ccaaaagtac cgttccaaca aaaccagac 350
315 tgtggcagtg gcagccggac ggagctgggt ggccattcct cgggaacagc 400
317 tcaccatgtc tgacaaactc cttgtctggg gcactaaggc aggcagcct 450
319 ctctggcccc ccgtcttctg gaacctagaa acccaaatga agccaaacgc 500
321 ccccggctg ggcctgacg tggacttttc cgaggatgac cccctggagg 550
323 ccactgtcca ttgggccccca cctacatggc catctcataa agttctgac 600
325 tgccagttcc actaccgaag atgtcaggag gcggcctgga cctgctgga 650
327 accggagctg aagaccatac ccctgacccc tgttgagatc caagatttg 700
329 agctagccac tggctacaaa gtgtatggcc gctgccgat ggagaaagaa 750
331 gaggatttgt gggcgagtg gagccccatt ttgtccttcc agacaccgcc 800
333 ttctgtctca aaagatgtgt gggatcagg gaacctctgt gggacgcctg 850
335 gaggagagga acctttgctt ctatggaagg cccagggcc ctgtgtgcag 900
337 gtgagctaca aagtctggtt ctgggttga ggtcgtgagc tgagtccaga 950
339 aggaattacc tgctgtgct ccctaattcc cagtggggcg gagtgggcca 1000
341 ggggtgtccg tgtcaacgcc acaagctggg agcctctcac caacctctct 1050
343 ttggtctgct tggattcagc ctctgcccc cgtagcgtgg cagtcaagcag 1100
345 catcgttgg agcacggagc tactggtgac ctggcaaccg gggcctgggg 1150
347 aaccactgga gcatgtagt gactgggctc gagatgggga cccctggag 1200
349 aaactcaact ggtccggct tccccctggg aacctcagt ctctgttacc 1250
351 agggaatttc actgtcgggg tccccctatc aatcactgt accgcagtct 1300
353 ctgcttcagg cttggcctct gcatectccg tctgggggtt caggaggaa 1350
355 ttagcaccac tagtggggcc aacgcttttg cgactccaag atgcccctcc 1400
357 agggaccccc gccatagcgt ggggagaggt cccaaggcac cagcttcgag 1450
359 gccacctcac ccactacacc ttgtgtgcac agagtggaac cagcccctcc 1500
361 gtctgcatga atgtgagtg caacacacag agtgtcacc tgctgacct 1550
363 tccttgggg cctgtgagc tgtgggtgac agcatctacc atcgtggac 1600
365 agggccctcc tgggtccatc ctccggttc atctaccaga taacaccctg 1650
367 aggtgaaaag ttctgccgg catcctattc ttgtgggct tgttctgtt 1700
369 ggggtgtggc ctgagcctgg ccacctctgg aagtgctac cacctaaggc 1750
371 acaaagtgt gccccgctgg gtctgggaga aagttcctga tcctgccaac 1800
373 agcagttcag gccagcccca catggagcaa gtacctgagg cccagcccct 1850

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/29/2002
PATENT APPLICATION: US/10/088,950A TIME: 12:34:31

Input Set : A:\Pl748R1E.txt
Output Set: N:\CRF3\08292002\J088950A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2433

VERIFICATION SUMMARY

DATE: 08/29/2002

PATENT APPLICATION: US/10/088,950A

TIME: 12:34:31

Input Set : A:\P1748R1E.txt

Output Set: N:\CRF3\08292002\J088950A.raw

L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2400